

Atty. Dkt. No. 039386-0112  
(PF-0662 USN)

### AMENDMENTS TO THE SPECIFICATION

Please replace the title at page 1 with the following rewritten title:

**"HUMAN ZINC FINGER RELATED PROTEINS"**

Please replace paragraph starting at page 14, lines 1-21 with the following rewritten paragraph:

Alternatively, a suite of commonly used and freely available sequence comparison algorithms is provided by the National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST) (Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410), which is available from several sources, including the NCBI, Bethesda, MD, and on the Internet at <http://www.ncbi.nlm.nih.gov/BLAST/>. The BLAST software suite includes various sequence analysis programs including "blastn," that is used to align a known polynucleotide sequence with other polynucleotide sequences from a variety of databases. Also available is a tool called "BLAST 2 Sequences" that is used for direct pairwise comparison of two nucleotide sequences, "BLAST 2 Sequences" and can be accessed, and used interactively at <http://www.ncbi.nlm.nih.gov/ncf/b12.html>, for example, from the NCBI. The "BLAST 2 Sequences" tool can be used for both blastn and blastp (discussed below). BLAST programs are commonly used with gap other parameters set to default settings. For example, to compare two nucleotide sequences, one may use blastn with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such default parameters may be, for example:

*Matrix: BLOSUM62*

*Reward for match: 1*

*Penalty for mismatch: -2*

*Open Gap: 5 and Extension Gap: 2 penalties*

*Gap x drop-off: 50*

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*Expect: 10*

*Word Size: 11*

*Filter: on*